SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited

<120> A Screening Method

<130> 3172WOOP

<150> JP 2003-122464

<151> 2003-04-25

<160> 15

<210> 1
<211> 453
<212> PRT
<213> Human

<400> 1

```
Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp
                  5                  10                  15
His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
              20                  25                  30
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn
          35                  40                  45
Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
      50                  55                  60
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
65                  70                  75                  80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
                  85                  90                  95
Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
              100                 105                 110
Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
          115                 120                 125
Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
      130                 135                 140
Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
145                 150                 155                 160
Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
                  165                 170                 175
Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
              180                 185                 190
Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
          195                 200                 205
Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
      210                 215                 220
Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe
225                 230                 235                 240
Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
                  245                 250                 255
Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
              260                 265                 270
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
          275                 280                 285
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
      290                 295                 300
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
305                 310                 315                 320
Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
                  325                 330                 335
Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
              340                 345                 350
Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
```

```
              355                 360                 365
Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
    370                 375                 380
Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
385                 390                 395                 400
Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
                405                 410                 415
Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
                420                 425                 430
Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
        435                 440                 445
Gln Glu His Glu Val
        450
```

<210> 2
<211> 1359
<212> DNA
<213> Human

<400> 2
```
atggcttcac ccagcctccc gggcagtgac tgctcccaaa tcattgatca cagtcatgtc   60
cccgagtttg aggtggccac ctggatcaaa atcaccctta ttctggtgta cctgatcatc  120
ttcgtgatgg gccttctggg gaacagcgcc accattcggg tcacccaggt gctgcagaag  180
aaaggatact tgcagaagga ggtgacagac cacatggtga gtttggcttg ctcggacatc  240
ttggtgttcc tcatcggcat gcccatggag ttctacagca tcatctggaa tcccctgacc  300
acgtccagct acaccctgtc ctgcaagctg cacactttcc tcttcgaggc ctgcagctac  360
gctacgctgc tgcacgtgct gacactcagc tttgagcgct acatcgccat ctgtcacccc  420
ttcaggtaca aggctgtgtc gggaccttgc caggtgaagc tgctgattgg cttcgtctgg  480
gtcacctccg ccctggtggc actgcccttg ctgtttgcca tgggtactga gtaccccctg  540
gtgaacgtgc ccagccaccg gggtctcact tgcaaccgct ccagcacccg ccaccacgag  600
cagcccgaga cctccaatat gtccatctgt accaacctct ccagccgctg gaccgtgttc  660
cagtccagca tcttcggcgc cttcgtggtc tacctcgtgg tcctgctctc cgtagccttc  720
atgtgctgga acatgatgca ggtgctcatg aaaagccaga agggctcgct ggccgggggc  780
acgcggcctc cgcagctgag gaagtccgag agcgaagaga gcaggaccgc caggaggcag  840
accatcatct tcctgaggct gattgttgtg acattggccg tatgctggat gcccaaccag  900
attcggagga tcatggctgc ggccaaaccc aagcacgact ggacgaggtc ctacttccgg  960
gcgtacatga tcctcctccc cttctcggag acgttttttct acctcagctc ggtcatcaac 1020
ccgctcctgt acacggtgtc ctcgcagcag tttcggcggg tgttcgtgca ggtgctgtgc 1080
tgccgcctgt cgctgcagca cgccaaccac gagaagcgcc tgcgcgtaca tgcgcactcc 1140
accaccgaca gcgcccgctt tgtgcagcgc ccgttgctct cgcgtcccg gcgccagtcc 1200
tctgcaagga gaactgagaa gatttctta agcactttc agagcgaggc cgagccccag 1260
tctaagtccc agtcattgag tctcgagtca ctagagccca actcaggcgc gaaaccagcc 1320
aattctgctg cagagaatgg ttttcaggag catgaagtt                         1359
```

<210> 3
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 3
tgtgacattg gccgtatgct   20

<210> 4
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 4
cagtcgtgct tgggtttgg   19

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 5
tgcccaacca gattcggagg atca   24

<210> 6

<211> 456
<212> PRT
<213> Mouse

<400> 6

| Met | Ala | Ser | Ser | Ser | Gly | Ser | Asn | His | Ile | Cys | Ser | Arg | Val | Ile | Asp |
| | | | 5 | | | | | 10 | | | | | 15 | | |

Met Ala Ser Ser Ser Gly Ser Asn His Ile Cys Ser Arg Val Ile Asp
              5   10   15
His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
              20   25   30
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Val Gly Ile Leu Gly Asn
              35   40   45
Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
              50   55   60
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
65   70   75   80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
              85   90   95
Asn Pro Leu Thr Thr Pro Ser Tyr Ala Leu Ser Cys Lys Leu His Thr
              100   105   110
Phe Leu Phe Glu Thr Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
              115   120   125
Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Lys Tyr Lys
              130   135   140
Ala Val Ser Gly Pro Arg Gln Val Lys Leu Leu Ile Gly Phe Val Trp
145   150   155   160
Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Ile
              165   170   175
Glu Tyr Pro Leu Val Asn Val Pro Thr His Lys Gly Leu Asn Cys Asn
              180   185   190
Leu Ser Arg Thr Arg His His Asp Glu Pro Gly Asn Ser Asn Met Ser
              195   200   205
Ile Cys Thr Asn Leu Ser Asn Arg Trp Glu Val Phe Gln Ser Ser Ile
210   215   220
Phe Gly Ala Phe Ala Val Tyr Leu Val Val Leu Ala Ser Val Ala Phe
225   230   235   240
Met Cys Trp Asn Met Met Lys Val Leu Met Lys Ser Lys Gln Gly Thr
              245   250   255
Leu Ala Gly Thr Gly Pro Gln Leu Gln Leu Arg Lys Ser Glu Ser Glu
              260   265   270
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
              275   280   285
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
              290   295   300
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Thr Tyr Phe Arg
305   310   315   320
Ala Tyr Met Ile Leu Leu Pro Phe Ser Asp Thr Phe Phe Tyr Leu Ser
              325   330   335
Ser Val Val Asn Pro Leu Leu Tyr Asn Val Ser Ser Gln Gln Phe Arg
              340   345   350
Lys Val Phe Trp Gln Val Leu Cys Cys Arg Leu Thr Leu Gln His Ala
              355   360   365

```
Asn Gln Glu Lys Arg Gln Arg Ala Arg Phe Ile Ser Thr Lys Asp Ser
    370             375             380
Thr Ser Ser Ala Arg Ser Pro Leu Ile Phe Leu Ala Ser Arg Arg Ser
385             390             395             400
Asn Ser Ser Ser Arg Arg Thr Asn Lys Val Phe Leu Ser Thr Phe Gln
                405             410             415
Thr Glu Ala Lys Pro Gly Glu Ala Lys Pro Gln Pro Leu Ser Pro Glu
            420             425             430
Ser Pro Gln Thr Gly Ser Glu Thr Lys Pro Ala Gly Ser Thr Pro Glu
        435             440             445
Asn Ser Leu Gln Glu Gln Glu Val
    450             455
```

<210> 7

<211> 1368
<212> DNA
<213> Mouse

<400> 7
```
atggcttcat ccagtggctc caaccacatc tgctcccgtg tcatcgatca tagccatgtt     60
cctgaatttg aggtggccac ttggatcaaa atcaccctca tcttggtgta cctgatcatt    120
tttgtggtag gcatcttggg caacagcgtc accatcaggg ttacgcaggt attgcagaag    180
aagggctatt tgcagaagga ggtgacagat cacatggtca gtttggcttg ttcagatatc    240
ttggtctttt tgattggcat gcccatggag ttctacagca tcatttggaa cccccctgacc   300
acacccagct atgctctgtc ctgtaagctc cacacgttcc tctttgagac gtgcagctac    360
gccacactgc tgcacgtgct gaccctcagc tttgagcgct acattgccat ttgtcatccc    420
ttcaagtata aagcagtgtc tggacctcgc caggtgaaac tgctgattgg ctttgtatgg    480
gtcacctccg ccctggtggc actgcctttg ctctttgcca tgggtatcga gtaccctctg    540
gtaaacgtac ccactcacaa gggactcaac tgcaacctct ctcgcacccg ccaccacgat    600
gaacctggaa actccaatat gtccatctgc acgaacctct ccaaccgttg ggaggtcttc    660
cagtccagca tctttggggc ctttgctgtt tacctggtgg tcctggcgtc tgtggctttc    720
atgtgttgga atatgatgaa agtgctaatg aagagcaagc agggcactct tgcagggacc    780
gggccacagc tccagctgag gaagtcagag agtgaggaga gccggacagc aagaagacag    840
accatcatat tcctgagact gattgtggtg acgttggccg tgtgttggat gcccaatcag    900
atccgacgga tcatggctgc agcaaaaccc aaacatgact ggaccagaac gtacttcagg    960
gcatacatga tcctcctgcc cttctctgat accttcttct acctcagctc tgtggtcaac   1020
cctctcctct acaacgtgtc ctctcagcag ttccggaagg tgttctggca ggtgctctgc   1080
tgccgcctga ctctgcagca tgccaaccaa gagaaacgcc agcgtgcccg cttcatctcc   1140
accaaggaca gcaccagctc agcccgcagc cccctcatct tcctagcctc ccggcgcagt   1200
aactcttcct ccaggagaac taacaaggtt ttcttaagca cttttcagac tgaggccaag   1260
cctggagagg ctaagcccca gcccttgagt cctgagtcac cacagactgg ctcagagacc   1320
aaaccagctg ggtccacccc agaaaatagt ttacaggagc aggaagta              1368
```

<210> 8

<211> 456
<212> PRT
<213> Rat

<400> 8
```
Met Ala Ser Ser Ser Gly Ser Ser Asn Ile Cys Ser Arg Val Ile Asp
                5               10              15
His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
            20              25              30
Leu Thr Leu Val Tyr Leu Ile Val Phe Val Val Gly Ile Leu Gly Asn
        35              40              45
Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
    50              55              60
Gln Lys Glu Val Thr Asp His Met Ile Ser Leu Ala Cys Ser Asp Ile
65              70              75              80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
            85              90              95
Asn Pro Leu Thr Thr Pro Ser Tyr Ala Leu Ser Cys Lys Leu His Thr
            100             105             110
```

```
Phe Leu Phe Glu Thr Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
        115                 120                 125
Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
        130                 135                 140
Asp Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
145                 150                 155                 160
Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Ile
                165                 170                 175
Glu Tyr Pro Leu Ala Asn Val Pro Thr His Lys Gly Leu Asn Cys Asn
                180                 185                 190
Leu Ser Arg Thr Arg His His Asp His Pro Gly Asp Ser Asn Met Ser
        195                 200                 205
Ile Cys Thr Asn Leu Ser Ser Arg Trp Glu Val Phe Gln Ser Ser Ile
        210                 215                 220
Phe Gly Ala Phe Ala Val Tyr Leu Val Val Leu Val Ser Val Ala Phe
225                 230                 235                 240
Met Cys Trp Asn Met Met Lys Val Leu Met Lys Ser Lys Arg Gly Thr
                245                 250                 255
Leu Ala Gly Thr Gly Pro Gln Leu Gln Leu Arg Lys Ser Glu Ser Glu
                260                 265                 270
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
        275                 280                 285
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
        290                 295                 300
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Lys Ser Tyr Phe Lys
305                 310                 315                 320
Ala Tyr Met Ile Leu Leu Pro Phe Ser Asp Thr Phe Phe Tyr Leu Ser
                325                 330                 335
Ser Val Val Asn Pro Leu Leu Tyr Asn Val Ser Ser Gln Gln Phe Arg
                340                 345                 350
Lys Val Phe Trp Gln Val Leu Cys Cys Arg Leu Thr Leu Gln His Ala
        355                 360                 365
Asn Gln Glu Lys Gln Gln Arg Ala Tyr Phe Ser Ser Thr Lys Asn Ser
        370                 375                 380
Ser Arg Ser Ala Arg Ser Pro Leu Ile Phe Leu Ala Ser Arg Arg Ser
385                 390                 395                 400
Asn Ser Ser Ser Arg Arg Thr Asn Lys Val Phe Leu Ser Thr Phe Gln
                405                 410                 415
Ala Glu Ala Lys Pro Leu Glu Gly Glu His Gln Pro Leu Ser Pro Glu
                420                 425                 430
Ser Pro Gln Thr Gly Ser Glu Thr Lys Pro Ala Gly Ser Ala Thr Glu
        435                 440                 445
Asn Ser Leu Gln Glu Gln Glu Val
450                 455
```

<210> 9

<211> 1368
<212> DNA
<213> Rat

<400> 9
```
atggcttcat ccagtggctc cagcaacatc tgctcccgag tcatcgatca cagccatgtc      60
cctgagttcg aagtggccac ttggatcaaa atcaccctca ccttggtgta cctgatcgtc     120
ttcgtggtag gcatcttggg caatagcgtc accatccggg ttacgcaggt attgcagaaa     180
aagggctatt tgcagaagga ggtgacagat cacatgatca gtttggcttg ttcagatatc     240
ttggtctttt tgattggcat gcccatggag ttctacagca tcatctggaa cccctgacc     300
acacccagct atgctctgtc ctgcaagctc cacacgttcc tctttgagac gtgtagctac     360
gccacattgc tgcatgtgct gaccctcagc tttgagcgct acattgccat ttgtcatccc     420
ttcagatata aggacgtgtc tggaccttgc caggtgaaac tgctgatcgg ctttgtatgg     480
gtcacctccg ctctggtggc actgcccttg ctctttgcca tgggtattga gtaccctctg     540
gcgaacgtcc ccactcacaa gggactcaac tgtaacctct ctcgtacccg ccaccacgat     600
catcctggag actccaatat gtccatctgc acgaacctct ccagccgttg ggaggtcttc     660
cagtccagca tctttggggc cttcgctgtt tacctggtgg tcctggtgtc tgtggctttc     720
atgtgttgga acatgatgaa agtgctaatg aagagcaagc ggggtactct ggcagggacc     780
```

```
ggaccacagc tgcagctgcg gaagtcagag agtgaggaga gccggacagc gagaagacag      840
accatcatat tcctgagact gatcgtggtg acactggccg tgtgttggat gccaaatcag      900
atccgacgga tcatggccgc agcaaaaccc aaacatgact ggaccaagtc gtacttcaag      960
gcgtacatga tcctcctccc cttctccgac accttcttct acctcagctc cgtggtcaac     1020
cctctcctct acaacgtgtc ttctcagcag ttccggaagg ttttctggca ggttctctgc     1080
tgccggctga ctctgcagca tgccaaccag gagaaacagc agcgtgccta cttcagctct     1140
accaaaaaca gcagccgctc agcccgaagc ccgctcatct tcctagcctc ccggcgtagt     1200
aactcttcct cccggagaac taacaaggtt ttcttaagca cttttcaggc ggaggctaag     1260
cctctagagg gcgagcacca gcccttgagt cctgagtcac cacagaccgg ctcagagacc     1320
aaacctgctg gttccgccac agaaaatagt ttacaggagc aggaagt                   1368
```

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 10
cccatggagt tctacagcat cat   23

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
tgtggagctt gcaggacaga   20

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 12
tggaaccccc tgaccacacc ca   22

<210> 13

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
gtacccactc acaagggact caac   24

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14

tattggagtt tccaggttca tcgt   24

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
caacctctct cgcacccgcc a   21